

AMENDMENTS TO THE CLAIMS

1. (Cancelled)
2. The method of claim 1, wherein the ~~high fidelity~~ L1 element comprises a sequence is at least about 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
3. (Currently amended) The A method of identifying candidate genes involved in claim 1, ~~wherein the complex disease is selected from the group consisting of systemic lupus erythematosus (SLE), multiple sclerosis, insulin dependent diabetes mellitus, rheumatoid arthritis, pemphigus, psoriasis, autoimmune thyroid disease, scleroderma, mixed connective tissue disease, polymyositis, dermatomyositis, Sjögren's syndrome, pemphigoid, vitiligo, primary biliary cirrhosis, chronic active hepatitis, Crohn's disease, ulcerative colitis, pernicious anemia, schizophrenia, and Alzheimer disease~~ comprising identifying a region of the genome adjacent to a disease-associated marker, and selecting any gene in the region containing an L1 element in an intronic region or in a 5' or 3' regulatory region as a candidate gene involved in SLE.
- 4-18. (Cancelled)
19. (New) The method of claim 2, comprising selecting any gene containing an L1 element in an intronic region as a candidate gene involved in SLE.
20. (New) The method of claim 2, comprising selecting any gene containing an L1 element in a 5' regulatory region as a candidate gene involved in SLE.
21. (New) The method of claim 2, comprising selecting any gene containing an L1 element in a 3' regulatory region as a candidate gene involved in SLE.
22. (New) The method of claim 2, wherein the L1 element has at least about 98% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.

23. (New) The method of claim 2, wherein the L1 element has at least about 99% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.

24. (New) The method of claim 2, wherein the distance between the first nucleotide of the L1 element and the first nucleotide of the gene is less than about 200,000 base pairs.

25. (New) The method of claim 2, wherein the distance between the first nucleotide of the L1 element and the first nucleotide of the gene is less than about 100,000 base pairs.